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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:08:31 ; Search time 16.6154 Seconds
(Without alignments)
209.686 Million cell updates/sec

Title: US-09-231-422d-2

Perfect score: 426
Sequence: 1 SVSEIQMLNHLGKHLNSMR.....KSLGEADKADVNVLTKAKSQ 84

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

: 1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	426	100.0	115	1	PTHY_HUMAN
2	419	98.4	115	1	PTH_MACP
3	375	88.0	115	1	PTHY_CANFA
4	365	85.7	115	1	PTHY_BOVIN
5	364	85.4	115	1	PTHY_PIG
6	317	74.4	115	1	PTHY_RAT
7	183.5	43.1	119	1	PTHY_CHICK
8	74.5	17.5	824	1	SVL_THEMEA
9	72	16.9	1257	1	RBL1_HUMAN
10	66	15.5	429	1	DDP2_ORYSA
11	65	15.3	443	1	HSLO_VIBCH
12	65	15.3	992	1	FLT3_MOUSE
13	65	15.3	1244	1	MIX1_CAEL
14	65	15.3	1388	1	RPOD_TOHAC
15	65	15.3	1937	1	MYH8_HUMAN
16	64.5	15.1	642	1	UL25_HSV6Z
17	64	15.0	632	1	FLID_CAMJE
18	63.5	14.9	1270	1	ITN1_XENLA
19	63.5	14.9	1270	1	ITN1_XENLA
20	63	14.8	456	1	DDP2_ARATH
21	62.5	14.7	205	1	KCUA_CHLPH
22	62.5	14.7	1658	1	ITN2_MOUSE
23	62	14.6	1033	1	VIT4_CAEL
24	62	14.6	1033	1	V328_MYCPN
25	62	14.6	1041	1	DD16_HUMAN
26	62	14.6	1084	1	MYSS_RABIT
27	62	14.6	1935	1	MTSS_CITCA
28	62	14.6	1938	1	MYH4_RABIT
29	62	14.6	1940	1	MYH4_RABIT
30	61.5	14.4	366	1	YE05_HAEIN
31	61.5	14.4	370	1	YA44_HELPY
32	61.5	14.4	378	1	UI25_HSV6G
33	61.5	14.4	555	1	UI25_HSV6U

34	61	14.3	910	1	HUL5_YEAST
35	61	14.3	1157	1	YE56_CAEL
36	60.5	14.2	707	1	RHO_SRLT
37	60.5	14.2	928	1	KINH_NEUCR
38	60.5	14.2	942	1	PKL1_HUMAN
39	60.5	14.2	1027	1	KINN_MOUSE
40	60.5	14.2	1032	1	KINN_HUMAN
41	60.5	14.2	1721	1	ITN1_HUMAN
42	60.5	14.2	1972	1	MYH8_HUMAN
43	60	14.1	455	1	MYH6_MOUSE
44	60	14.1	465	1	MYH6_MOUSE
45	60	14.1	1172	1	SVK2_MYCTU

ALIGNMENTS

RESULT 1	PTHY_HUMAN	STANDARD:	PRT:	115 AA.
ID	PTHY_HUMAN			
AC	P01270:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).			
GN	PTH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82150870: PubMed=6950381;			
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;			
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid			
RT	hormone.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).			
RP	[2]			
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RX	MEDLINE=83169834: PubMed=6320408;			
RA	Vasilek T.J., McDevitt B.E., Freeman M.W., Fennick B.J.,			
RT	Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;			
RT	"Nucleotide sequence of the human parathyroid hormone gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).			
RN	[3]			
RP	SEQUENCE OF 26-37.			
RX	MEDLINE=74174967: PubMed=4833516;			
RA	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;			
RT	"Structural analysis of human parathyroid hormone by a new			
RT	microsequencing approach.";			
RL	Nature 249:155-157(1974).			
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RP	SEQUENCE OF 32-68.			
RX	MEDLINE=74111656: PubMed=4521809;			
RA	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,			
RT	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;			
RT	"The amino-acid sequence of the amino-terminal 37 residues of human			
RT	parathyroid hormone.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).			
RN	[5]			
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RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,			
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RT	Biochemistry 17:5723-5729(1978).			
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RT	Biochemistry 17:5723-5729(1978).			
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RT	"Complete amino acid sequence of human parathyroid hormone.";			
RT	Biochemistry 17:5723-5729(1978).			
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RT	Biochemistry 17:5723-5729(1978).			
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RT	"Complete amino acid sequence of human parathyroid hormone.";			
RT	Biochemistry 17:5			

[7]
 RP REVISIONS.
 RX MEDLINE-75146516; PubMed-1125201;
 RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
 RT "A reinvestigation of the amino-terminal sequence of human
 RL parathyroid hormone.";
 RN Biochemistry 14:1842-1847(1975).
 (8)
 RP SYNTHESIS OF 32-65.
 RX MEDLINE-75059220; PubMed-4474131;
 RA Tregear G.W., van Rietschoten J., Green E., Niall H.D.,
 RA Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
 RT "Solid-phase synthesis of the biologically active N-terminal 1-34
 RL peptide of human parathyroid hormone.";
 RN Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
 (9)
 RP SYNTHESIS OF 32-65.
 RX MEDLINE-73227467; PubMed-4721748;
 RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
 RA Rinkler B., Rittel W., Sieber P.;
 RT "Synthesis of sequence 1-34 of human parathyroid hormone.";
 RN Helv. Chim. Acta 56:470-473(1973).
 (10)
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE-91299748; PubMed-2069952;
 RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wengender E., Mayer H.;
 RT "Investigation of the solution structure of the human parathyroid
 RL hormone fragment (1-34) by IH NMR spectroscopy, distance geometry,
 RN and molecular dynamics calculations.";
 RN Biochemistry 30:6936-6942(1991).
 (11)
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE-93345518; PubMed-8344299;
 RA Barden J.A., Cutbertson R.M.;
 RT "Stabilized NMR structure of human parathyroid hormone(1-34).";
 RN Eur. J. Biochem. 215:315-321(1993).
 (12)
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE-95318084; PubMed-7797503;
 RA Marx U.C., Austermann S., Bayer P., Adermann K., Eichart A.,
 RA Slicht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
 RA Roesch P.;
 RT "Structure of human parathyroid hormone 1-37 in solution.";
 RN J. Biol. Chem. 270:15194-15202(1995).
 (13)
 RP STRUCTURE BY NMR OF 32-70.
 RX MEDLINE-20090619; PubMed-10623601;
 RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
 RT "Solution structures of human parathyroid hormone fragments
 RL hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
 RT hPTH(1-37).";
 RN Biochem. Biophys. Res. Commun. 267:213-220(2000).
 (14)
 RP VARIANT ARG-18.
 RX MEDLINE-91009811; PubMed-2212001;
 RA Arnold A., Horst S.A., Gargella T.J., Baba H., Levine M.A.,
 RA Kronenberg H.M.;
 RT "Mutation of the signal peptide-encoding region of the
 RL preproparathyroid hormone gene in familial isolated
 RT hypoparathyroidism.";
 RN J. Clin. Invest. 86:1084-1087(1990).
 (15)
 RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FTH).
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC
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 CC DR EMBL, V00597; CAA23843.1;
 CC DR EMBL, A29146; CAA01956.1;
 CC DR PIR, A01536; PTHU.
 CC DR PIR, A19338; A19339.
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 CC DR MIM, 168450;
 CC DR InterPro: IPR001415; Parathyrd_hrm.
 CC DR InterPro: IPR003625; Pthyrhorm_sub.
 CC DR Pfam: PF01279; Parathyroid.1.
 CC DR ProDom: PD01687; Pthyrhorm_sub.1.
 CC DR SMART, SM00087; PTH.1.
 CC DR PROSITE, PS00335; PARATHYROID.1.
 CC KW Hormone; Signal; Disease mutation; 3D-structure.
 CC FT SIGNAL 1 25
 CC FT PROPEP 32 31
 CC FT CHAIN 36 115
 CC FT VARIANT 18 18
 CC
 CC PARATHYROID HORMONE.
 CC C-> R (IN FTH; LEADS TO INEFFICIENT
 CC PROCESSING OF THE PRECURSOR).
 CC /ftid-var_006047.
 CC N-> D (IN REF. 5).
 CC SQ SEQUENCE 115 AA; 12661 MW; 849015736A6E5597 CRC64;

 CC Query Match 100.0%; Score 426; DB 1; Length 115;
 CC Best Local Similarity 100.0%; Pred. No. 4,4e-40;
 CC Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 CC QY 1 SVSEQLMHNHNGKHLNSRVEMLRKKLDVNFVALGAPLAPRAGSORPRKKEDNVLY 60
 CC DB 32 SVSEQLMHNHNGKHLNSRVEMLRKKLDVNFVALGAPLAPRAGSORPRKKEDNVLY 91
 CC QY 61 ESHEKSLGEADKADYVNLTKAKSQ 84
 CC DB 92 ESHEKSLGEADKADYVNLTKAKSQ 115

 CC RESULT 2
 CC PTH_MACFA STANDARD; PRT; 115 AA.
 CC ID PTH_MACFA
 CC AC 09XT35;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Parathyroid hormone precursor (Parathyrin) (PTH).
 CC GN PTH.
 CC OS Macaca fascicularis (Cebus eating macaque) (Cynomolgus monkey).
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC CC Cercopithecoidea; Macaca.
 CC OX NCBI_TaxID:9541;
 CC OX 11
 CC RP SEQUENCE FROM N.A.
 CC RA Malaviatitmond S., Takenaka O.;
 RT "Nucleotide sequences of parathyroid gene in five species of macaque
 RT of Thailand.";
 RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC -----

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DR EMBL: A0130257; AAD42777.1; -;
DR HSSP: P01270; 1HPY.
DR InterPro: IPR001415; Parathyrd_hrm.
DR InterPro: IPR003625; Pthyrdorm_sub.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyrdorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
DR Hormone; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SEQUENCE 115 AA; 12890 MW; 8C250DEF24BE5597 CRC64;

Query Match 98.4%; Score 419; DB 1; Length 115;
Best Local Similarity 96.4%; Pred. No. 2.6e-39;
Matches 81; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIOLMNLGKHLNLSMERVEWLRKKLDVNFVALGAPLAPRDAGSQRPKKEDNVLY 60
DB 32 SVSEIOLMNLGKHLNLSMERVEWLRKKLDVNFVALGAPLAPRDAGSQRPKKEDNVLY 91
QY 61 ESHEKSLGEADKADVNLTKAKSQ 84
DB 92 ESHEKSLGEADKADVNLTKAKSQ 115

RESULT 3
PTHY_CANFA
ID PTHY_CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;

[1]
SEQUENCE FROM N.A.
RC TISSUE=Parathyroid;
RA MEDLINE=95369696; PubMed=7642102;
RA Rosol T.J., Steimeyer C.L., McCauley L.K., Greene A.,
RA Demille J.W., Capen C.C.;
RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
RT protein and parathyroid hormone.";
RL Gene 160:241-243(1995).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL: U15662; AAA82584.1; -;
DR HSSP: P01268; 12WC.
DR InterPro: IPR001415; Parathyrd_hrm.
DR InterPro: IPR003625; Pthyrdorm_sub.

DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyrdorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
DR Hormone; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;

Query Match 88.0%; Score 375; DB 1; Length 115;
Best Local Similarity 88.1%; Pred. No. 1.8e-34;
Matches 74; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 SVSEIOLMNLGKHLNLSMERVEWLRKKLDVNFVALGAPLAPRDAGSQRPKKEDNVLY 60
DB 32 SVSEIOLMNLGKHLNLSMERVEWLRKKLDVNFVALGAPLAPRDAGSQRPKKEDNVLY 91
QY 61 ESHEKSLGEADKADVNLTKAKSQ 84
DB 92 ESHEKSLGEADKADVNLTKAKSQ 115

RESULT 4
PTHY_BOVIN
ID PTHY_BOVIN STANDARD; PRT; 115 AA.
AC P01268;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;

[1]
SEQUENCE FROM N.A.
RX MEDLINE=8005617; PubMed=388425;
RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathan J., Sharp P.A.,
RA Potts J.T., Jr., Rich A.;
RT "Cloning and nucleotide sequence of DNA coding for bovine
RT preproparathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=82037785; PubMed=6170060;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Introduction by molecular cloning of artifactual inverted sequences
RT at the 5' terminus of the sense strand of bovine parathyroid hormone
RT cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=83105964; PubMed=6185374;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL Mol. Cell. Endocrinol. 28:411-424(1982).
RN [4]
SEQUENCE FROM N.A.
RX MEDLINE=84262483; PubMed=6086460;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
RT parathyroid hormone.";
RL Gene 28:319-329(1984).
RN [5]
SEQUENCE OF 26-115.

RX MEDLINE=74142666; PubMed=4522780;
RA Hamilton J.W., Miall H.D., Jacobs J.W., Keutmann H.T., Potts J.T., Jr.,
RA Cohn D.V.;
RT "The N-terminal amino-acid sequence of bovine preproparathyroid
RT hormone.";

Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).

SEQUENCE OF 32-115.

MEDLINE-71076162; PubMed-5531031;

Mall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
Aurbach G.D., Potts J.T. Jr.;
"The amino acid sequence of bovine parathyroid hormone I.";
Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).

SEQUENCE OF 32-115.

MEDLINE-71063634; PubMed-5275384;

Brewer H.B. Jr., Roman R.;
"Bovine parathyroid hormone: amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).

SYNTHESIS OF 32-65.

MEDLINE-71091588; PubMed-4322265;

Potts J.T. Jr., Tregear G.W., Keutmann H.T., Mall H.D., Sauer R.,
Defeo L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
"Synthesis of a biologically active N-terminal tetraoctapeptide
of parathyroid hormone.";
Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).

STRUCTURE BY NMR OF 32-68.

MEDLINE-20090619; PubMed-10623601;

Marx U.C., Ademann K., Bayer P., Forssmann W.-G., Rosch P.;
"Solution structures of human parathyroid hormone fragments
hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
bPTH(1-37)." ;
Biochem. Biophys. Res. Commun. 267:213-220(2000).

-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.

-1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

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EMBL: V00106; CAA23439.1; -
EMBL: J00024; AAA30747.1; -
EMBL: K01938; AAA30749.1; -
EMBL: M25082; AAA30748.1; -
PIR: A01534; PTBO.
PIR: A24949; A24949.
PDB: 1ZWC; 12-MAR-97.
InterPro: IPR001415; Parathyrd_hrm.
InterPro: IPR003625; Pthythorm_sub.
Pfam: PF01279; Parathyroid.1.
DR PRODOM: PD010687; Pthythorm_sub; 1.
DR SMART: SM00087; PTH.1
DR PROSITE: PS00335; PARATHYROID.1.
DR KMW Hormone; Signal; 3D-structure.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12960 MW; 2ED246B348880710 CRC64;

Query Match 85.7%; Score 365; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 2.2e-33;
Matches 72; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 SVSEIQLMHNKGLHNSREYEMLRKKLQDVHNFVALGAPLAPRAGSGRPKKEDNVLY 60
DB 32 SVSEIQLMHNKGLHNSREYEMLRKKLQDVHNFVALGASLIVHDGSSQRPKKEDNVLY 91

OY 61 ESHEKSLGEADKADVNVLTAKSQ 84
DB 92 ESHKSLGEADKADVNVLTAKSQ 115

RESULT 5

ID	PTHY_PIG	STANDARD;	PRT;	115 AA.
AC	P01269;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Parathyroid hormone precursor (Parathyrin) (PTH).			
GN	PTH.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-87316938; PubMed-3628009;			
RA	Schmelzer H.-J., Gross G., Widera G., Mayer H.;			
RT	"Nucleotide sequence of a full-length cDNA clone encoding preparathyroid hormone from pig and rat." ; Nucleic Acids Res. 15:6740-6740(1987).			
RL	[2]			
RN	SEQUENCE OF 26-115.			
RP	MEDLINE-76018954; PubMed-1164500;			
RX	Chu L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.;			
RA	"Porcine parathyroid hormone. Identification, biosynthesis, and partial amino acid sequence." ; Biochemistry 14:3631-3635(1975).			
RL	[3]			
RN	SEQUENCE OF 32-115.			
RX	MEDLINE-7425317; PubMed-4840833;			
RA	Sauer R.T., Mall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H., Potts J.T. Jr.; "The amino acid sequence of porcine parathyroid hormone." ; Biochemistry 13:1994-1999(1974).			
RL	[4]			
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.			
CC	-1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.			
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CC	----- EMBL: X05722; CAA29193.1; - PIR: A01535; PTPG. PIR: B26806; B26806. HSSP: P01270; 1BMX. InterPro: IPR001415; Parathyrd_hrm. InterPro: IPR003625; Pthythorm_sub. Pfam: PF01279; Parathyroid.1. DR PRODOM: PD010687; Pthythorm_sub; 1. DR SMART: SM00087; PTH.1 DR PROSITE: PS00335; PARATHYROID.1. DR KMW Hormone; Signal. FT SIGNAL 1 25 FT PROPEP 26 31 FT CHAIN 32 115 FT CONFLICT 106 106 V -> G (IN REF. 4). SQ SEQUENCE 115 AA; 12852 MW; 9FE8BCDE51ABAC16 CRC64;			
Query Match	85.4%;	Score 364;	DB 1;	Length 115;
Best Local Similarity	85.7%;	Pred. No. 2.9e-33;		
Matches	72;	Conservative 5;	Mismatches 7;	Indels 0; Gaps 0;
OY	1 SVSEIQLMHNKGLHNSREYEMLRKKLQDVHNFVALGAPLAPRAGSGRPKKEDNVLY 60			
DB	32 SVSEIQLMHNKGLHNSREYEMLRKKLQDVHNFVALGASLIVHDGSSQRPKKEDNVLY 91			
OY	61 ESHEKSLGEADKADVNVLTAKSQ 84			

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DB      92 ESHOKSLGEGDRAADVLYLAKPO 115

RESULT 6
PTHY_RAT STANDARD: PRT; 115 AA.
AC      P04089; 063473;
DT      01-NOV-1986 (Rel. 03, Created)
DT      01-NOV-1986 (Rel. 03, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Parathyroid hormone precursor (Parathyrin) (PTH).
GN      PTH.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      NCBI_TaxID=10116;
RP      SEQUENCE FROM N.A.
MEDLINE-84135846; PubMed-6321505;
Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
"Gene encoding parathyroid hormone. Nucleotide sequence of the rat
gene and deduced amino acid sequence of rat preproparathyroid
hormone.";
J. Biol. Chem. 259:3320-3329(1984).
RN      (2)
RP      SEQUENCE FROM N.A.
MEDLINE-87316938; PubMed-3628009;
Schmelzer H.-J., Gross G., Wildera G., Mayer H.;
"Nucleotide sequence of a full-length cDNA clone encoding
preproparathyroid hormone from pig and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
RN      (3)
RP      SEQUENCE OF 10-115 FROM N.A.
TISSE-Parathyroid;
Schmelzer H.J., Gross G., Mayer H.;
"Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
hormone.";
Adv. Gene Technol. 21:228-229(1984).
RN      (4)
RP      SEQUENCE OF 32-115 FROM N.A.
STRAIN-Sprague-Dawley; TISSE-Brain, Parathyroid, and Liver;
MEDLINE-96079910; PubMed-7388314;
Nutley M.T., Parlmi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger
ribonucleic acid.";
Endocrinology 136:5600-5607(1995).
RN      (1)
RP      FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
CC      -1- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.
CC      -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: K01268; AAA41979.1; -
CC      EMBL: X05721; CA629192.1; -
CC      EMBL: M54875; AAA57156.1; -
CC      EMBL: S80127; -; NOT_ANNOTATED_CDS.
CC      PIR: A05091; A05091.
CC      PIR: A26806; A26806.
CC      HSSP: P01270; 12WB.
CC      InterPro: IPR001415; Parathyrd_hrm.
CC      InterPro: IPR003625; Pthythorm_sub.
CC      Pfam: PF01279; Parathyroid.1.
CC      ProDom: PD010687; Pthythorm_sub; 1.
CC      SMART: SM00087; PTH; 1.
CC      PROSITE: PS00335; PARATHYROID; 1.

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KW      Hormone; Signal:
FT      SIGNAL 1 25
FT      PROPEP 26 31
FT      CHAIN 32 115
FT      CONFLICT 18 18
FT      CONFLICT 23 23
FT      CONFLICT 33 33
FT      CONFLICT 62 62
SQ      SEQUENCE 115 AA; 12722 MW; 7B434CFC528B230 CRC64;

Query Match
Best Local Similarity 74.4%; Score 317; DB 1; Length 115;
Matches 61; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY      1 SVSEIDLMNHLKRLNSMERVEMLRKKLDVNFVALGARLAPRDAGSORPKKEDNVLV 60
DB      32 AVSEIDLMNHLKRLNSMERVEMLRKKLDVNFVALGARLAPRDAGSORPKKEDNVLV 91
QY      61 ESHOKSLGEGDRAADVLYLAKSQ 84
DB      92 DGNKSLGEGDRAADVLYLAKSQ 115

RESULT 7
PTHY_CHICK STANDARD: PRT; 119 AA.
AC      P15743;
DT      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Parathyroid hormone precursor (PTH).
OC      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      (1)
RP      SEQUENCE FROM N.A.
MEDLINE-89219100; PubMed-2710135;
Russell J., Sherwood L.M.;
"Nucleotide sequence of the DNA complementary to avian (chicken)
preproparathyroid hormone mRNA and the deduced sequence of the
hormone precursor.";
Mol. Endocrinol. 3:325-331(1989).
RN      (2)
RP      SEQUENCE FROM N.A.
MEDLINE-89284968; PubMed-3251402;
Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
Kronenberg H.M.;
"Nucleotide sequence of cloned cDNAs encoding chicken
preproparathyroid hormone.";
J. Bone Miner. Res. 3:689-698(1988).
RN      (1)
RP      FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
CC      -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: M31604; AAA49093.1; -
CC      EMBL: M36522; AAB02866.1; -
CC      PIR: A34937; A34937.
CC      HSSP: P01270; 1HPY.
CC      InterPro: IPR001415; Parathyrd_hrm.
CC      InterPro: IPR003625; Pthythorm_sub.
CC      Pfam: PF01279; Parathyroid.1.
CC      ProDom: PD010687; Pthythorm_sub; 1.
CC      SMART: SM00087; PTH; 1.

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DR PROSITE: PS00335; PARATHYROID. 1.
 KW Hormone; Signal. 1.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 119
 SQ SEQUENCE 119 AA; 13943 MW; B309D8E772997FEE CRC64;
 Query Match
 Best Local Similarity 43.1%; Score 183.5; DB 1; Length 119;
 Matches 44; Conservative 13; Mismatches 17; Indels 21; Gaps 2;
 QY 1 SVSEIOLNHNKGLHNSERVEVLEKRLQDYHNFVALGAPLAPRAGSQRPKKEDNLY 60
 DB 32 SVSEIOLNHNKGLHNSERVEVLEKRLQDYHNFVALGAPLAPRAGSQRPKKEDNLY 60
 QY 61 E-----SHEKSLGEADKADNVNLTAK 82
 DB 84 EIRNRLLPEHLRAAVOKKSIDLCKAVNVLFKTK 118
 RESULT 8
 ID SYL_THEME STANDARD; PRT; 824 AA.
 AC Q9WY15;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (Leurs).
 GN LEUS OR TM0168.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
 OC Thermotogaceae; Thermotoga.
 OX NCBI_TaxID-2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MSB8 / DSM 3109;
 RX MEDLINE-99287316; PubMed-10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher C.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of Thermotoga maritima.";
 RL Nature 399:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: ATP + L-Leucine + tRNA(Leu) = AMP +
 diphosphate + L-leucyl-tRNA(Leu).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 CC -----
 CC EMBL: AE001702; AAD35261.1;
 DR TIGR: TM0168;
 DR InterPro: IPR002302; Leu-tRNA-synthla.
 DR InterPro: IPR002300; tRNA-synt_1a.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR Pfam: PF00133; tRNA-synt.1.1.
 DR PRINTS: PRO0095; TRNASYNTHLEU.
 DR TIGRPFAM: TIGR00396; LeuS_bact.1.
 DR PROSITE: PS00178; AA-TRNA_Ligase_I.1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 41 51 "HIGH" REGION.
 FT SITE 580 584 "WMSKS" REGION.
 FT BINDING 583 583 ATP (BY SIMILARITY).

SQ SEQUENCE 824 AA; 95624 MW; 7CB0252A76A844EC CRC64;
 Query Match
 Best Local Similarity 17.5%; Score 74.5; DB 1; Length 824;
 Matches 21; Conservative 26; Mismatches 24; Indels 19; Gaps 4;
 QY 5 IOLNHNKGLHNSERVEVLEKRLQDYHNFVALGAPLAPRAGSQRPKKEDNLY 60
 DB 692 MELVNHLSQYLNVSYPQEGEMKRLRELVEKTLTALSFAPHLAEFPHDGN-----D 744
 QY 57 NVLVE-----SHEKSLGEADKADNVNLTAK 82
 DB 745 SLVVOQSWPSYDPKALVEVEVEIATQNGK 774
 RESULT 9
 ID RBB1_HUMAN STANDARD; PRT; 1257 AA.
 AC P29374; Q15991; Q15992; Q15993;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Retinoblastoma-binding protein 1 (RBBP-1).
 GN RBBP1 OR RBP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM I).
 RC MEDLINE-94020841; PubMed-8414517;
 RA Pattay A.R., Helin K., Dembski M.S., Dyson N., Harlow E.,
 RA Vuocolo G.A., Hanbik M.G., Haskell K.M., Olfiff A., Defeo-Jones D.,
 RA Jones R.E.;
 RT "Characterization of the retinoblastoma binding proteins RBP1 and
 RBP2.";
 RL Oncogene 8:3149-3156(1993).
 RN [2]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE-93205410; PubMed-8455946;
 RA Otterson G.A., Klatzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
 RT "Alternative splicing of the RBP1 gene clusters in an internal exon
 RT that encodes potential phosphorylation sites.";
 RL Oncogene 8:949-957(1993).
 RN [3]
 RP SEQUENCE OF 855-1203 FROM N.A. (ISOFORM I).
 RX MEDLINE-91312450; PubMed-1857421;
 RA Defeo-Jones D., Huang P.S., Jones R.E., Haskell K.M., Vuocolo G.A.,
 RA Hanbik M.G., Huber H.E., Olfiff A.;
 RT "Cloning of cDNAs for cellular proteins that bind to the
 RT retinoblastoma gene product.";
 RL Nature 352:251-254(1991).
 CC -1- FUNCTION: INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE
 CC RETINOBLASTOMA PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; I (shown here), II and III; are
 CC produced by alternative splicing.
 CC -----
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 CC -----
 CC EMBL: S66427; AAB28543.1;
 DR EMBL: S57153; AAB25833.1;
 DR EMBL: S57160; AAB25834.1;
 DR EMBL: S57162; AAB25835.2;
 DR PIR: S16953; S16953.
 DR Genew: HGNC:9885; RBBP1.
 DR MIM: 180201;

DR InterPro: IPR001606; ARID.
 DR InterPro: IPR000953; Chromo.
 DR InterPro: IPR002999; Tudor.
 DR Pfam: PF01388; ARID; 1.
 DR SMART: SM00501; BRIGAT; 1.
 DR SMART: SM00298; CHROMO; 1.
 DR SMART: SM00333; TUDOR; 1.
 KM Trans-acting factor; Nuclear protein; Alternative splicing.
 FT DOMAIN 951 964
 FT RETINOBLASTOMA PROTEIN BINDING
 FT (POTENTIAL).
 FT VARSPIC 1106 1174 MISSING (IN ISOFORM III).
 FT VARSPIC 1175 1175 N -> D (IN ISOFORM III).
 FT VARSPIC 1121 1174 MISSING (IN ISOFORM III).
 FT CONFLICT 385 385 L -> V (IN REF. 2).
 FT CONFLICT 618 618 S -> R (IN REF. 2).
 FT CONFLICT 653 653 K -> V (IN REF. 2).
 FT CONFLICT 779 779 A -> T (IN REF. 2).
 FT CONFLICT 1178 1178 D -> S (IN REF. 3).
 FT CONFLICT 1196 1201 IRKYM -> SEITICL (IN REF. 3).
 FT SEQUENCE 1257 AA; 142666 MW; F3C0ABD6DE43DC CRC64;

Query Match 16.9%; Score 72; DB 1; Length 1257;
 Best Local Similarity 26.8%; Pred. No. 5.9;
 Matches 19; Conservative 21; Mismatches 27; Indels 4; Gaps 2;

OY 14 HUNSMERVELARKKODVHN-FVALGAPLAPDAGSQRPKKEDNVLVESHERSLGEADK 72
 DB 1179 NMSTIRISLQKQEIERYKYSKSEVATIDRRKRLKKDREV---SHAGSMSSAS 1235

OY 73 ADVNVLTKAKS 83
 DB 1236 SDGMSPPSSS 1246

RESULT 10
 ID DP2L_ORYSA STANDARD; PRT; 429 AA.
 AC 09LRES: 09SNL2; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE DNA polymerase delta small subunit (EC 2.7.7.7).
 GN POL2
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 NCBI_TaxID=4530;

[1]
 SEQUENCE FROM N.A.
 RA Hatanaka M., Kimura S., Sakaguti K.;
 RT "Oryza sativa DNA polymerase delta small subunit."
 RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Saeki T., Matsunoto T., Yamamoto K.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THE FUNCTION OF THE SMALL SUBUNIT IS NOT YET CLEAR.
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
 CC + [DNA](N).
 CC -1- SUBUNIT: HETERODIMER WITH SUBUNITS OF 125 KDA AND 50 KDA (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE DELTA/II SMALL SUBUNIT
 CC FAMILY.

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 CC -----
 DR EMBL: AB037900; BAA99574.1; -
 DR EMBL: AP000615; BAA85393.1; -
 KM Transferrase; DNA-directed DNA polymerase; DNA replication;
 KM Nuclear protein.
 FT CONFLICT 256 256 Q -> QVS (IN REF. 2).
 FT CONFLICT 411 414 LMLR -> VNTSCMLTGKALFYLC (IN REF. 2).
 FT CONFLICT 418 429 CSTLSPSTFEDA -> SYKRAKSSGD (IN REF. 2).
 SO SEQUENCE 429 AA; 48000 MW; 10BA6ED519EBB67 CRC64;

Query Match 15.5%; Score 66; DB 1; Length 429;
 Best Local Similarity 28.4%; Pred. No. 7.6;
 Matches 23; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

OY 6 QLMHNIGKHSNEREMRLKKODVHNVALGAPLAPDAGSQRPKKEDNVLVES--H 63
 DB 318 QNIDDLTKYSDAKDKLEFERTLRHRL-----APTAAPSLSQY-PYTDKDFLVESCPH 371

OY 64 EKSLGEADRADVNVLTAKSQ 84
 DB 372 VYFVGNDKYEFGQLGLEKQ 392

RESULT 11
 ID HSLU_VIBCH STANDARD; PRT; 443 AA.
 AC 09KN07;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE ATP-dependent hsl protease ATP-binding subunit hslu.
 GN HSLU OR VC2674.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 NCBI_TaxID=66;

[1]
 SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eilen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Niernan W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae."
 RL Nature 406:477-483(2000).

CC -1- FUNCTION: CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION
 CC COMPLEX (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH HSLV (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.

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CC EMBL: AE004333; AAF5815.1; -
 CC HSSP: P32168; ID02.

DR TIGR: VC2674; ID02.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003959; AAA_ATPase_centre.
 DR InterPro: IPR004491; Hsp_HsluV.
 DR Pfam: PF00004; AAA; 1.
 DR SMART: SM00382; AAA; 1.
 DR TIGRFAMS: TIGR00390; hslu; 1.

KW Chapterone: ATP-binding; Complete proteome.
 FT NP_BIND 57 64 ATP (POTENTIAL).
 SQ SEQUENCE 443 AA; 49900 MW; DAEL3E82FAB6A38F CRC64;
 Query Match 15.3%; Score 65; DB 1; Length 443;
 Best Local Similarity 29.7%; Pred. No. 10;
 Matches 19; Conservative 13; Mismatches 30; Indels 2; Gaps 1;
 QY 14 HLNSEMEVRLRKLDQVHFAVLGAPLAPRAGSQPRKEDNVLVESHEKSLGEADKA 73
 DB 112 HQAMEKVFRAELAEERVLADLLP--PRDAGQAQKQENSTNQVFRKKUREQQLN 169
 QY 74 DVNV 77
 DB 170 DKEL 173
 RESULT 12
 FLT3_MOUSE STANDARD; PRT; 992 AA.
 ID FLT3_MOUSE 000342;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FL cytokine receptor precursor (EC 2.7.1.112) (tyrosine-protein kinase receptor flk-2) (fetal liver kinase 2) (tyrosine-protein kinase FLT3).
 GN FLT3 OR FLT-3 OR FLK-2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91292518; PubMed=1648448;
 RA Matthews W., Jordan C.T., Wiegand G.W., Pardoll D., Lemischka I.R.,
 RT "A receptor tyrosine kinase specific to hematopoietic stem and progenitor cell-enriched populations.",
 RL Cell 65:1143-1152(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92019834; PubMed=1656368;
 RA Rosnet O., Marchetto S., Delapeyriere O., Birnbaum D.,
 RT "Murine Flt3, a gene encoding a novel tyrosine kinase receptor of the PDGFR/CSF1r family.",
 RL Oncogene 6:1641-1650(1991).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=93203405; PubMed=8384358;
 RA Marot N., Rottapel R., Rosnet O., Marchetto S., Lavezzl C.,
 RT "Biochemical characterization and analysis of the transforming potential of the FLT3/FLK2 receptor tyrosine kinase.",
 RL Oncogene 8:909-918(1993).
 CC -1- FUNCTION: RECEPTOR FOR THE FL CYTOKINE. HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HEMATOPOIETIC STEM AND PROGENITOR CELL-ENRICHED POPULATIONS. FOUND IN BRAIN, PLACENTA AND TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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DR EMBL: M64689; AAA37634.1; -;
 DR EMBL: X59398; CAA42041.1; -;
 DR PIR: A39931; A39931.
 DR HSSP: P1362; 1FGK.
 DR MGD: MGT:95559; Flt3.
 DR InterPro: IPR00719; Euk_pkinase.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001824; RTK_naseII.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 2.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00219; TYRC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00240; RECEPTOR_TYR_KIN_ITI; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR Signal: Transferrase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
 FT CHAIN 1 27
 FT DOMAIN 28 992
 FT TRANSMEM 545 564
 FT DOMAIN 565 992
 FT NP_BIND 611 946
 FT NP_BIND 617 625
 FT BINDING 645 645
 FT ACT_SITE 814 814
 FT CARBOHYD 44 44
 FT CARBOHYD 133 133
 FT CARBOHYD 152 152
 FT CARBOHYD 307 307
 FT CARBOHYD 324 324
 FT CARBOHYD 352 352
 FT CARBOHYD 445 445
 FT CARBOHYD 474 474
 FT CARBOHYD 503 503
 FT CARBOHYD 542 542
 FT CONFLICT 150 150
 FT CONFLICT 242 242
 FT CONFLICT 726 726
 FT CONFLICT 957 979
 FT CONFLICT 983 983
 SQ SEQUENCE 992 AA; 112639 MW; 407A08785372100 CRC64;
 Query Match 15.3%; Score 65; DB 1; Length 992;
 Best Local Similarity 21.7%; Pred. No. 26;
 Matches 28; Conservative 17; Mismatches 32; Indels 52; Gaps 4;
 QY 2 VSEIQMLNHLGKHLNM-----ERYEWLKKLQDV----- 31
 DB 660 MSELKMTHTLGHNDIVNLGACTLSGPVYLIFCYCCYDLDNLVLSKREKRTWTETIF 719
 QY 32 --HNF-----VALGAPLAPRAGSQPRKEDNVLVESHEKSLGEA 70
 DB 720 KEHNSSYTFQAHSSNMPGSHREVOLHPDLQLSGFNNSIHSDEIYE-NOKRLAE 778
 QY 71 DRADVAVLT 79
 DB 779 EEDDLNVL 787
 RESULT 13
 MIXI_CAEEL STANDARD; PRT; 1244 AA.
 ID MIXI_CAEEL 009591;
 AC 009591;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitotic chromosome and X-chromosome associated protein mix-1.


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GN MIX-1 OR M106.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98117254; PubMed=9458050;
RA Lieb J.D., Albrecht M.R., Chuang P.T., Meyer B.J.;
RT "Mix-1: an essential component of the C. elegans mitotic machinery
RT executes X chromosome dosage compensation.";
RN Cell 92:265-277(1998).
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Palmer S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Required for X-chromosome dosage compensation. Member of
CC the dosage compensation complex that associates specifically with
CC hermaphrodite X chromosomes to reduce their gene expression during
CC interphase.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
CC FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY.
CC -----
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CC -----
DR EMBL: U96387; AAC47834.1;
DR EMBL: Z46935; CAA87054.1;
DR EMBL: AL031266; CAA20330.1;
DR EMBL: Z46794; CAA20330.1; JOINED.
DR EMBL: Z46935; CAA20330.1; JOINED.
DR EMBL: Z46794; CAA86786.1;
DR EMBL: AL031266; CAA86786.1; JOINED.
DR EMBL: Z46935; CAA86786.1; JOINED.
DR WormRep: M106.1; CE18083
DR InterPro: IPR003405; SMC_C.
DR InterPro: IPR003395; SMC_N.
DR Pfam: PF02463; SMC_N; 1.
DR Pfam: PF02483; SMC_C; 1.
DR ProDom: PD000006; ABC_transport; 1.
ATP-binding: Coiled coil; Nuclear protein.
NP_BIND 32
NP_BIND 39
FT DOMAIN 245 350 COILED COIL (POTENTIAL).
FT DOMAIN 415 479 COILED COIL (POTENTIAL).
FT DOMAIN 702 1043 COILED COIL (POTENTIAL).
FT DOMAIN 1109 1135 ALA/ASP-RICH (NA-BOX).
FT DOMAIN 1239 1242 POLY-ASP.
SO SEQUENCE 1244 AA; 140341 MW; 255FD9C3D8C6AA9 CRC64;

Query Match 15.3%; Score 65; DB 1; Length 1244;
Best Local Similarity 26.8%; Pred. No. 34;
Matches 22; Conservative 16; Mismatches 34; Indels 10; Gaps 2;

QY 7 LHMNLGRHLSMR-----VENLRKKLDYVNFALCAPLAPRDAGSQRPKKEDNVLES 62
DB 756 VVADLVHSEERKNOAELEATVTKLDEDKIKTLESKMKNDKNSQERKKKLTALLOK 815

QY 63 HE-----KSLGEADKADYVNL 78
DB 816 ABOCTVANKNRGKARREYWL 837

RESULT 14
RPOD_TOBAC STANDARD: PRT; 1388 AA.
ID RPOD_TOBAC STANDARD: PRT; 1388 AA.

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AC P38550;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN RPOC2.
OS Nicotiana tabacum (Common tobacco).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
ON NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bright yellow 4;
RA Shinzaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
RA Matsubayashi T., Zaita N., Chunmongse J., Obokata J.,
RA Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.-Y., Sugita M.,
RA Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
RA Tohdo N., Shimada H., Sugiyama M.;
RT "The complete nucleotide sequence of the tobacco chloroplast genome:
RT its gene organization and expression.";
RN EMBO J. 5:2043-2049(1986).
RL [2]
RN REVISIONS.
RX MEDLINE=94003079; PubMed=8400137;
RA Olmstead R.G., Sweere J.A., Wolfe K.H.;
RT "Ninety extra nucleotide in ndhF gene of tobacco chloroplast DNA: a
RT summary of revisions to the 1986 genome sequence.";
RL Plant Mol. Biol. 22:1191-1193(1993).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC {RNA}(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z00044; CAA77410.1; ALT_SEQ.
DR HSP: Q9KWT6; 1HOM.
DR InterPro: IPR000722; RNA_pol_A.
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF00623; RNA_pol_A; 1.
DR Pfam: PF01854; RNA_pol_A2; 2.
DR Transferrase: Transcription; DNA-directed RNA polymerase; Chloroplast.
SO SEQUENCE 1388 AA; 156840 MW; 41FD7F238913186C CRC64;

Query Match 15.3%; Score 65; DB 1; Length 1388;
Best Local Similarity 27.6%; Pred. No. 39;
Matches 16; Conservative 15; Mismatches 21; Indels 6; Gaps 2;

QY 20 RYEMLRKKLDYVNFALGAPLAPRDAGSQRPKKEDNVLESHEKSLGENDKADY 75
DB 1305 RIDWLKGLKEN-----VVLGGVLPVGTGFGVLVHPSKOHNNIPLETKKNLFGEGMDI 1358

RESULT 15
MYH8_HUMAN STANDARD: PRT; 1937 AA.
ID MYH8_HUMAN STANDARD: PRT; 1937 AA.
AC P13535; Q14910;
DT 01-JAN-1990 (Rel. 13, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Myosin heavy chain, skeletal muscle, perinatal (MyHC-perinatal).
GN MYH8.

```

OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=90333631; PubMed=2373371;
RA Karsch-Mizrachi I., Feghali R., Shows T.B. Jr., Lelwand L.A.;
RT "Generation of a full-length human perinatal myosin heavy-chain-
RL encoding cDNA";
RN Gene 89:289-294(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95324556; PubMed=7601129;
RA Tullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S.,
RT Steadman H.H., Rubinstein N.A.;
RT "Characterization of a human perinatal myosin heavy-chain
transcript";
RN Eur. J. Biochem. 230:1001-1006(1995).
RN [3]
RP SEQUENCE OF 502-1937 FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=90233862; PubMed=1691980;
RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
RT Arnold H.H.;
RT "Identification of three developmentally controlled isoforms of human
RN myosin heavy chains";
RN Eur. J. Biochem. 189:55-65(1990).
RN [4]
RP SEQUENCE OF 860-1937 FROM N.A.
RX MEDLINE=89234168; PubMed=2715179;
RA Feghali R., Lelwand L.A.;
RT "Molecular genetic characterization of a developmentally regulated
RN human perinatal myosin heavy chain";
RN J. Cell Biol. 108:1791-1797(1989).
RN [5]
RP SEQUENCE OF 1-46 FROM N.A.
RA Esser K., Tishar A., Myszkowski M.;
RT "Isolation and characterization of the human perinatal MHC promoter";
RN Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
RN [1]
RP FUNCTION: MUSCLE CONTRACTION.
CC [1]
CC SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC [1]
CC SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC [1]
CC PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
CC [1]
CC MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE
CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC SUBFRAGMENT (S2).
CC [1]
CC SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC [1]
CC SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC
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CC
CC EMBL; M36769; AAC17185.1;
CC EMBL; Z38133; CA86293.1;
CC DR EMBL; X51592; CA35941.1;
CC DR EMBL; AF067143; AAC21557.1;
CC PIR; A30220; A30220.
CC HSP; P13538; ZMYS.

DR Genew; HGNC:7578; MYH8.
DR MIM; 160741; -
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR001609; myosin_head.
DR Pfam; PF00063; myosin_head.
DR Pfam; PF00612; IQ_1.
DR Pfam; PF01576; Myosin_tail; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head.
DR SMART; SM00242; MYSC; 1.
DR SMART; PS50096; IQ; 1.
DR PROSITE; PS50096; IQ; 1.
KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW ATP-binding; Methylation; Alkylation; Multigene family;
KW Calmodulin-binding.
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